Comparison of MetAP2 Homologues (mouse = SEQ ID NO:13; rat = SEQ ID NO:17; human = SEQ ID NO:12; yeast = SEQ ID NO:14)

```
      1             15 16            30 31            45 46            60 61            75 76            90
mouse MAGVEQAASFGGHLN GDLDPDDREEGTSST AEEAAKKKRRKKKKG KGAVSAVQQELDKES GALVDEVAKQLESQA LEEKERDDDDEDGDG     90
rat   MAGVEEASSFGGHLN RDLDPDDREEGTSST AEEAAKKKRRKKKKG KGAVSAGQQELDKES GTSVDEVAKQLERQA LEEKEKDDDDEDGDG     90
human MAGVEEVAASGSHLN GDLDPDDREEGAAST AEEAAKKKRRKKKKS KGPSAAGEQEPDKES GASVDEVARQLERSA LEDKERDEDDEDGDG     90
yeast --------------- --------------- --------------- -------MTDAEIEN SPASDLKELNLENEG VEQQDQAKADESDPV     38

      91           105 106          120 121          135 136          150 151          165 166          180
mouse DADGATGKKKKKKKK KRGPKVQTDPPSVPI CDLYPNGVFPKGQEC EYPPTQDGRTAAWRT TSEEKKALDQASEEI WNDFREAAEAHRQVR    180
rat   DGDGAAGKKKKKKKK KRGPRVQTDPPSVPI CDLYPNGVFPKGQEC EYPPTQDGRTAAWRT TSEEKKALDQASEEI WNDFREAAEAHRQVR    180
human DGDGATGKKKKKKKK KRGPKVQTDPPSVPI CDLYPNGVFPKGQEC EYPPTQDGRTAAWRT TSEEKKALDQASEEI WNDFREAAEAHRQVR    180
yeast ESKKKKNKKKKKKKS N----------VKKI ELLFPDGKYPEGAWM DYHQDFNLQRTTDEE SRYLKRDLERA--EH WNDVRKGAEIHRRVR    116

      181          195 196          210 211          225 226          240 241          255 256          270
mouse KYVMSWIKPGMTMIE ICEKLEDCSRKLIKE NGLNAG-------LA FPTGCSLNNCAAHYT PNAGDTTVLQYDDIC KIDFGTHISGRIIDC    263
rat   KYVMSWIKPGMTMIE ICEKLEDCSRKLIKE NGLNAG-------LA FPTGCSLNNCAAHYT PNAGDTTVLQYDDIC KIDFGTHISGRIIDC    263
human KYVMSWIKPGMTMIE ICEKLEDCSRKLIKE NGLNAG-------LA FPTGCSLNNCAAHYT PNAGDTTVLQYDDIC KIDFGTHISGRIIDC    263
yeast RAIKDRIVPGMKLMD IADMIENTTRKYTGA ENLLAMEDPKSQGIG FPTGLSLNHCAAHFT PNAGDKTVLKYEDVM KVDYGVQVNGNIIDS    206

      271          285 286          300 301          315 316          330 331          345 346          360
mouse AFTVTFNPKYDILLT AVKDATNTGIKCAGI DVRLCDVGEAIQEVM ESYEVEIDGKTYQVK PIRNLNGHSIGPYRI HAGKTVPIVKGGEAT    353
rat   AFTVTFNPKYDILLK AVKDATNTGIKCAGI DVRLCDVGEAIQEVM ESYEVEIDGKTYQVK PIRNLNGHSIGPYRI HAGKTVPIVKGGEAT    353
human AFTVTFNPKYDTLLK AVKDATNTGIKCAGI DVRLCDVGEAIQEVM ESYEVEIDGKTYQVK PIRNLNGHSIGQYRI HAGKTVPIVKGGEAT    353
yeast AFTVSFDPQYDNLLA AVKDATYTGIKEAGI DVRLTDIGEAIQEVM ESYEVEINGETYQVK PCRNLCGHSIAPYRI HGGKSVPIVKNGDTT    296

      361          375 376          390 391          405 406          420 421          435 436          450
mouse RMEEGEVYAIETFGS TGKGVVHDDMECSHY MKNFDVGHVPIRLPR TKHLLNVINENFGTL AFCRRWLDRLGESKY LMALKNLCDLGIVDP    443
rat   RMEEGEVYAIETFGS TGKGVVHDDMECSHY MKNFDVGHVPIRLPR TKHLLNVINENFGTL AFCRRWLDRLGESKY LMALKNLCDLGIVDP    443
human RMEEGEVYAIETFGS TGKGVVHDDMECSHY MKNFDVGHVPIRLPR TKHLLNVINENFGTL AFCRRWLDRLGESKY LMALKNLCDLGIVDP    443
yeast KMEEGEHFAIETFGS TGRGYVTAGGEVSHY ARSAEDHQVMPTLDS AKNLLKTIDRNFGTL PFCRRYLDRLGQEKY LFALNNLVRHGLVQD    386

      451          465 466          480
mouse YPPLCDIKGSYTAQF EHTILLRPTCKEVVS RGDDY--     478
rat   YPPLCDIKGSYTAQF EHTILCAQPVKKLSA EEMTIKT     480
human YPPLCDIKGSYTAQF EHTILLRPTCKEVVS RGDDY--     478
yeast YPPLNDIPGSYTAQF EHTILLHAHKKEVVS KGDDY--     421
```

Figure 1

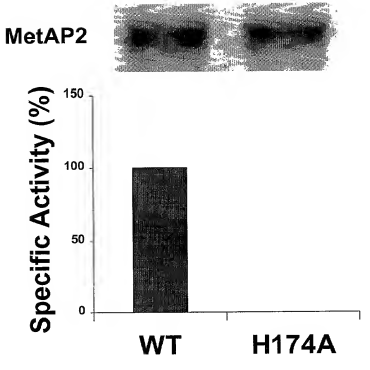
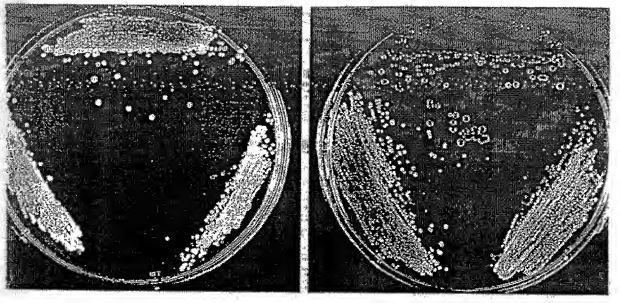


Figure 2



A. Glucose

B. Galactose

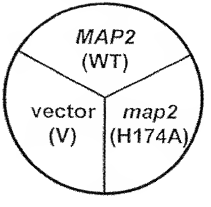


Figure 3

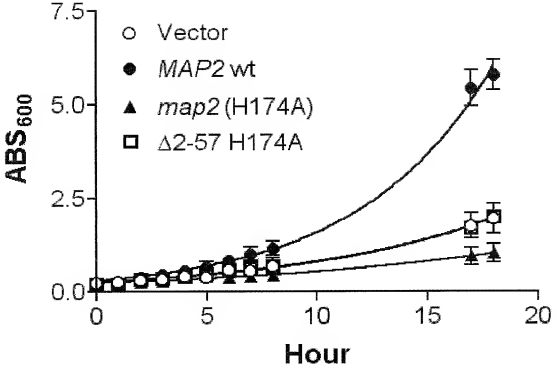
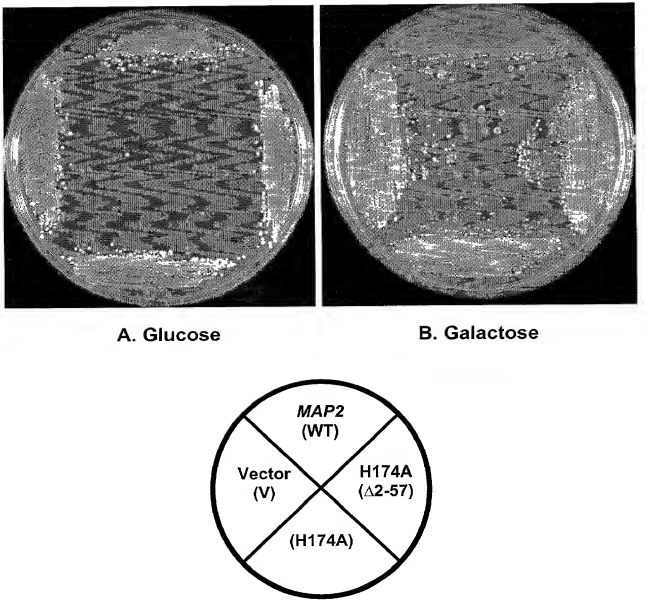
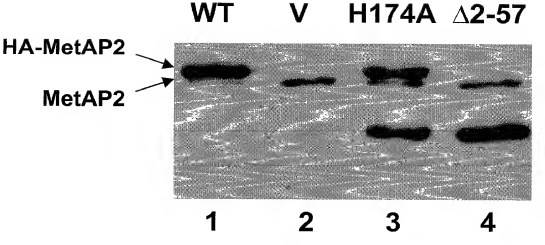

7.5
5.0
2.5
0.0
ABS600
Vector
MAP2 wt
map2 (H174A)
Δ2-57 H174A
0
5
10
15
20
Hour

Figure 4



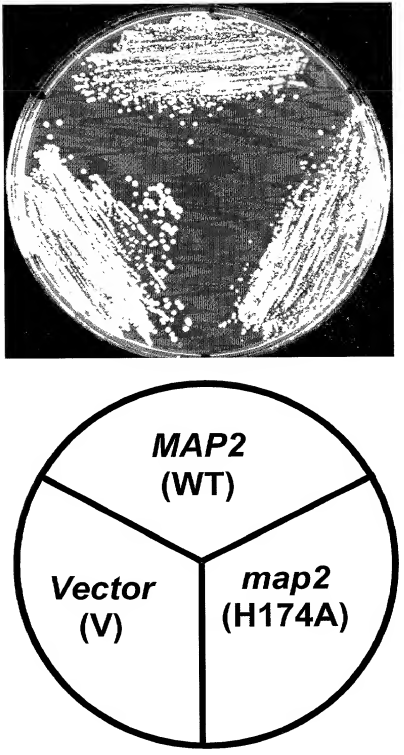
H174A-MetAP2 requires N-terminal residues 2-57 for inhibition of map1Δ growth under the GAL1 promoter.

Figure 5



The steady state levels of each MetAP2 construct are comparable. Immunoblot comparison of HA-MetAP2 wt, HA-MetAP2 H174A, and MetAP2 Δ2-57 H174A steady state levels in map1Δ.

Figure 6



Overexpression of H174A-MetAP2 under the GPD promoter does not inhibit the growth of map2Δ

Figure 7

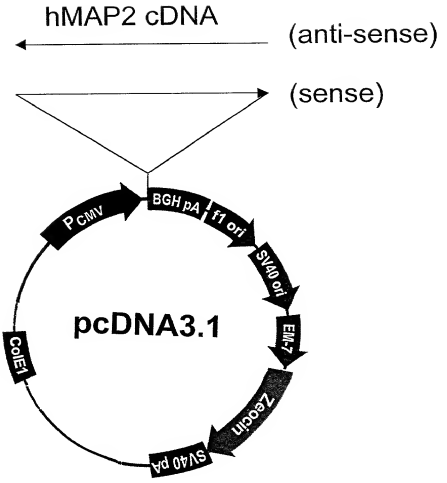

hMAP2 cDNA
(anti-sense)
(sense)
P CMV
BGH pA
f1 ori
SV40 ori
EM-7
Zeocin
SV40 pA
ColE1
pcDNA3.1

FIGURE 8

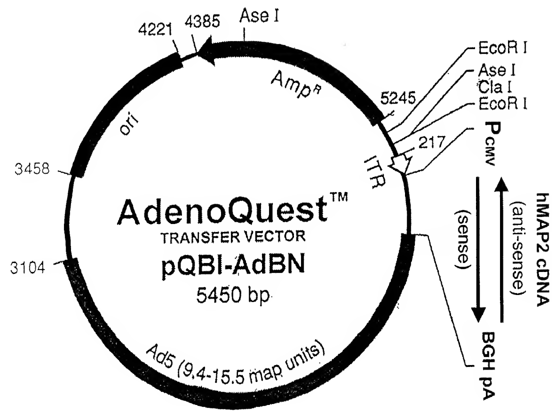

AdenoQuest™
TRANSFER VECTOR
pQBI-AdBN
5450 bp
Ase I
4221
4385
Amp^R
5245
EcoR I
Ase I
Cla I
EcoR I
217
ITR
P CMV
hMAP2 cDNA
(anti-sense)
(sense)
BGH pA
ori
3458
3104
Ad5 (9,4-15.5 map units)

FIGURE 9

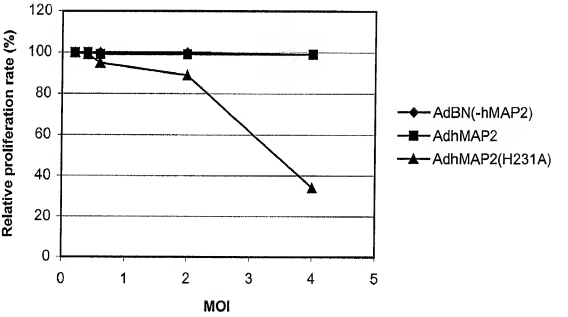

120
100
80
60
40
20
0
Relative proliferation rate (%)
0
1
2
3
4
5
MOI
AdBN(-hMAP2)
AdhMAP2
AdhMAP2(H231A)

Figure 10

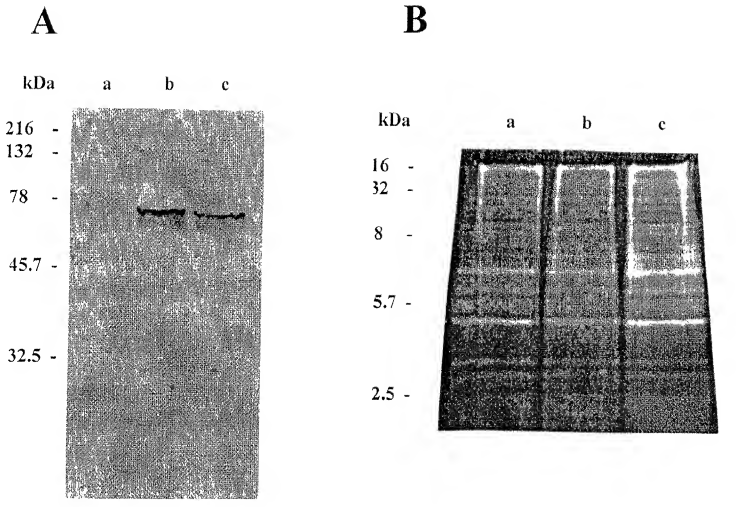


Figure 11